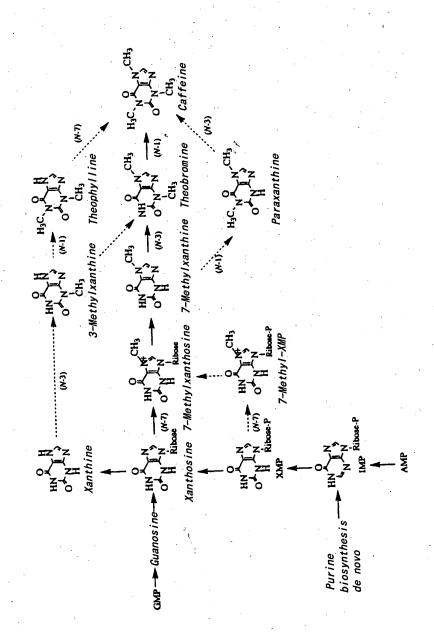
E: THEOBROMINE SYNTHASE POLYPEPTIDE OFFEE INVENTOR(S): HIROSHI SANO ET AL APPLICATION SERIAL NO: UNASSIGNED SHEET 1 of 6



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E: THEOBROMINE SYNTHASE POLYPEPTIDE

OFFEE T AND THE GENE ENCODING SAID POLYPEP

INVENTOR(S): HIROSHI SANO ET ALA
APPLICATION SERIAL NO: UNASSIGNED

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FIG. 2

ACTGGTTCTC AGTTGCAGAT GAAGAATGAA CTTCTACCGC CCCCGAGGAG CACTGCGAAC CACATTTTA GAATACCATG AATCTATACA TTATGATGCT GGCATCATTA GAATGCAGCA AAAGCTTGTT AAAGCTGTGTA	GCCAAGGTGG TTGGGATGCC TTAGGATGCC AAACTTGAGG TCCATGCATT AAAAGGAGCA AGGATGCGTT GACTTACTTG GCTTCAGTAG GCTTCTCTA ATTAGATCAG AAGGTTACTG ATTAGATCAG AAGGTTACTG ATTAGTTGGT ATTAGTTGGT ATTATTGGT	AACCTGTCCT CTCCGGACG CTCCCACCATTCA AAGAAAATGG TITTACACTC TITTACTCTTC CGGAAGAGTT AAGAAGCAAA TTGATGATGA TTTACGAACC GCTTGGGCAA TITTACGAACC	T TGAACAATGI A AGGTTTTCTG A AGGTAMATA TTCTTACAGI C CAAAGCAAGT T AAACGACTTCACGI A TTGCCAAGTA TTGCCAAGTA C CATCCTAGCA A GGGCTTCAT A AGGCTTCAT A TTGCCAAGTA C CATCCTAGCA A TGGGTTGTT	C GTACGGGAA T TTAACGGT G ACTGATCTT G GGATCGTGC CTTCAGTTT CCTCCGCCC G GTTGCTGAG G GTGCTGAG G AGGAGGAGAA AGATCCCAT AGTCATTT TCTGATTT TCTGATACGT TCTGATACGT TCTGATACGT TCTGATACGT TCTGATACGT TCTGATACGT TCTGATACGT TCTGATACGT TCTGATACGT TCTGATACGT	T TGTTGCGGGI T GGGACACTG T GGGACACTG T CTAAAATG T TATCCCAGG T TATCCCAGG G TCCAGAAGGG C TCCTTACTTG G GACGTCTGG G GTCCCAGTATA G GACAGCTATA TCCCAGTATA A TCATTTCTCT	C CAACTTGCC C ACAAGTAT A TTTCAATTC C AATGCCTGG T TCCCAGCGG C ATATTTGGA G GGAAGAAAA A AATTTATAA C CAGCGATGA T TATACCTGA C CACTGCGAAAAA C CACTGCGAAAAA C CACTGCGAAAAA C CACTGCGAAAAA C CACTGCGGTGA C CACTGCGGTTAACCTGAAAAA C CACTGCGGTTAACCTGAAAAAA C CACTGCGGTTAACCTGAAAAAA C CACTGCGGTTAACCTGAAAAAA C CACTGCGGTTAAAAAACCAACTGCGGTTAAAAAAACCAACTGCGGTTAAAAAAACCAACTGCGGTTAAAAAAACCAACTGCGGTTAAAAAACCAACTGCGGTTAAAAAACCAACTGCGGTTAAAAAACCAACTGCGGTTAAAAAACCAACTGCGGTTAAAAAACCAACTGCGGTTAAAAAACCAACTGCGGTTAAAAAACCAACTGCGGTTAAAAAACCAACTGCGGTTAAAAAACCAACTGCGGTTAAAAAACCAACTGCGGTTAAAAAACCAACTGCGGTTAAAAAACCAACTGCGGTTAAAAAACCAACTGCGGTTAAAAAAACAAAAAAAA	C AACATCAAC T GACAAAGTTT G GTTTTCATC T TTGGTGACTC T TGGTGACTC T CAGAGTGAAT A TTGGACAGTT C TTGCAGACT C TTGCAGACT C TTGCAGACT T CAGAGTT A CAGGAGTA C TGGAGAGT T GCAGACT T GGGTTCTAT	T CCTTCAATCA A AGTGCATTAA A AGCAAGAAAT TGCTGCCAAG G GGAGCTCTT AATTGGGGAT AAGATTTTAC TTAAGCTCCG CAGCGCATGT GGTTTGCCATG GGTTTGCATG CAGCGCATGT CAGCATGTT CAGCTCTAACA CCGAGTATTA CCGAGTATTA ATATTTTCAT	9 18 27 36 45 54 63 72 81 90 99 108 117 126 135
AAGCTACGCC CAACITACTCCC ACAAAGTATT TTTCAATTCG AATGCCTGGC TCCCAGCGGT ATATTTGGAT CATTTGCAAA GGAAGAAAAA ACGCGATGAC CAGCGATGAA TATACCTGAC TGCCAAAAAA	AAGAATTCAT AACATCAACA GACAAAGTTA GTITTCATGT TCTTTCCACG TTGGTGACTG CAATTTACGA GGACATGAAT TTGGACAGTT TTGGACAGTT TTGGAGACTT CATGCTACAG ATATTCCACA	CCTTCAATCA AGTGCATTAA GGCAGAAAAT TGCTGCCAAG GCAGACTCTT AATTGGGGAT AAGATTTTAC TCGACGGCCC TCAATGTTCC TTAAGCTCCG CAGCCATGT CAGCGCATGT CAGCGCATGT CAGCAGCATGT	ACTGGTTCTC AGTTGCGGAT GAAGAATGAA TTTCTACCGC CCCCGAGGAG CACTGCGAAC CACATTTTTA GAATACCATG AATCTATGCA TTATGATGCT GGCATCATTA GAATGCAGCA GAATGCAGCA AAAGCTTGTT	GCCAAGGTGA TTGGGATGCG TTAGAAACGTC AAACTTGACA TCAATGCATT AAAAGGAGCA AAGGATTCTTG GCTTCAGTAG GCTTCTCTA CTTAGATCAG AAGGTTATCC TATAGTTGGT	TCCAAGAAGT AACCTGTCCT CTTCCGGACC CCACCATTCA AAGAAATGG TITTACACTTC TTTACTCTTC CAGTGGGATT AAGAATTAAA TTGATGATCA TTTACGACC GCTTGGCAA TTTTTTTTTT	TGAACAATGC AAACACTT GGTTTTTCTG ACGCAAGATA TTCTTACAGT CAAAGCAAGT GCTTTCACGC AAACGATTT TTGCAATT TTGCCAAGTA ACTCCAAGTA ACTCCAAGTA ACTCCAAGTA ACTCCAAGTA ACTCCAACTA ACTCCAACTA ACTCCAACTA ACTCCAACTA ACTCCTCAACTA ACTCCTCAACTA ACTCCTCAACTA	GTAGGGGAAT TTAACAGTTC ACTGATCTTT GGATCGTGCC CTTCAATTTT CCTCCGCCCG GGCCGAATGC GTTGTTGAGG GAGGAGGAAG AGATCCCATT AATCATTTTG AATAATCTTA	TGTTGCGGGC GGGACATTGT TCCAAAATGA TAATAGCCGC TATCCCAGGT TCCAGAAGGC TCCTTACTTG GACATCTGGA GTTCTTTGA CCCCAGAATA GAGAAGCTAT TCATTTCTCT	92 188 276 366 456 540 636 726 816 900 998 1170 1260 11304
CAAGCTACGC CCAAGTAT ATTTCAATTC CAATGCCCGG CTCCTAGCGG CATATTTGGA GCATTTGTAA AGGAAGAAAA AAATTTATA CGGTTAGAGC CAAAGGTTCT CTTTTTGTGTT	CAAGAATTCA CAACATCAAC TGACAAAGTT TGACTTCTAC TTTGGTGACT TCAATTTACG AGGAGTTGAA ATTGGTAGAC AGTGAGAGTT AGTTTACGAA CCCCTTGGGC	GCCTACAATC AAGTGCATAA GGCCAGGAAA GTGCTGCCAA AGCAGACTCT GAATTGGGGA AAAGATTTTA TTAGACGCCC TTCAATCTTC TTTAAGGTCC CCCATCCTCG AAAGGCTTCT ATAAGTGCCC AAAGGCTTCT ATAAGTGCCC	AACTGGTTCT AAGTTGCGGA AGAAGAATGA GCTTCTACCG TCCCCGAGGA TCAGTACGAA CCACATTTCT GGAATGCCAT CAGTCTATAT TTTACGATGC CAAGTCATTA TTTACGATGC TAGAATATCT TTGGGGGGTCT	CGCCAAGGTG TTTGGGATGC AATTAGAACGT CAAACTTGAG GTCCATGCAT CAAAGGGAGC AAGGGTTCAT ACCTTCAGCA TGGCTTCTCT TATCATTCT TTCGGGTATT TTCGGGTATT TTCGGGTATT	CTCCAAGAAG AAACCTGTCC GCTICTGGAC CCCACCATIC AAAGAAATG TITITIACACT TITIGGAGAGGT GAGATGGCAA GAGAAGTAA ATTGAGATGA ATTGAGATGA ATTGAGATGA ATTGAGATGA TCGCCCAAAA GTGCTTTTTA	TTGAACAATG CAAACACACT AGATTTTTCT GACGCAAAAT CTTGTTACTG CCAAAGCAAG TGTTTTCACA TAAACGACTT AGTGCATAGT AGTGCATAGT AACTATTCAA ACATATTCAA AGCCAGAGAA	CGTACGGGAA TTTAACAGTT GAATGATCTT GATCGTCGCC TCGTCTGCCC TGGCCGAATG GGTTGTTGAG TGGGAGGAA TGAGGAGGAA CAGGTTTGCG GTCAGACGTG	TTGTTGCGGG CGGGACATTG TTCCCAAATG CTAATAGGGG TTATCTCAGG GTCCAGAAGG CTCCTTACTT GGACATCTGG GGTTCTTTTG GTTGCATCTT AAGCATGCAG TAAAAAGTTTG	90 180 270 360 450 540 630 720 810 990 1080 1170 1260 1316
GAATGCATCC CAACAAGTGC AGTTGGCCAG CAAGTTGCTG CTACGGCAGA GATTGAATTG TACGAAAGAT TGAATTCGAC TAGTTTCAAT GACTTTTAAG GACTTTAAAT TGCAGCAAAG GTTTGATTAATT TGCAGCAAAG GTTTGTTTTT	TACAATCTGG ATTAAAGTTG GAAGAGAAGA CCAAGCTTCT CTCTTCCCCG GGGATTGGTG TITACCACAT GAACCGAATC ATTCCATTCT GCCCATTATG GGATCAGTTT GTTCTCCACA	CTCTTGCCAA CGGATTTGGG ATGAATTAGA ACCGCAAACT CAAACAAAGG TTCTAAGGAT CCCTAGACTT TTACACCTTC ATGCTGCCTT TGGGCAAACG TGTGCCGTTG	GGTGAAACCT ATGGCTTCT ACGTCCCACC CGAGAAGAA GCATTITTG GAGTATTTAC TCATTCGAAA ACTTGACATG AGCAGAAGAA CTCTATTGAT CCTCGCAAGT CTGCTATAAT GGGGTCTTTC	TTCCTTGAAC GGACCAAACA ATTCAGATTT AATGGACGCA CACTCTTGTT TCTTCCAAAG GAGTTGTTTT GCAATAAACG GTAAAGTGCA GATGATTACCATTTGGAG AATCTTATCA	TGCATATGAA AATGCATACG CACTITITAAC TICTGAATGA AGATAGGATC ACAGTGTTCA CACGTGGTCC ACTIGATGA ACTIGATGA CAGTAGAGA CAGTAGAGAT CAGTAGAGT CAGTAGAGT TICTCTCCC GTTTTGTATT	AGAATTGTTG AGTGCGGGAC TCTTTTCCAA GTGCCTAATA TTGGTTATCT GCCCGTCCAG AATGCTCCTT TGAGGGACTT GGAAGGTTCT CCATGAACAA GCCTGACTAA CAAAAAAGCCA	CGGGCCAACT ATTGTGCAAA AATGATTTCA AGCGCAATGC CAGGTTCCCA AAGGCATATT ACCTGCATTT CTGGAGGAAG TGCGAAATTT ATTAAAGCAG GAGAACTCAG GAGAACTCAG	TGCCCAACAT GTATTGACAA ATTCGGCTCTTT GCGGTTTGGT TGGATCAATT GCGAACAATTGGA AAAAATTGGA TATATCTGGA AGTATGTGGC TTGCGAAGCA ACGTGAAAAA	90 180 270 360 450 540 630 720 810 990 1176 1260 1298

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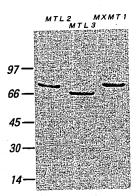
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FIG. 3

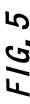
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MTL1	::::::::::::::::::::::::::::::::::::::	50
MTL2	::::::::::::::::::::::::::::::::::::::	50
MTL3	:::::::R::G::::::::::::SA::Q:V::::::V:::::V::::::	50
MXMT1	INKCIKVADLOCASCENTILIVRDIVQSIIKVOQEEKNELERETTQIFIN	99
MTL1	::::::::::::::::::::::::::::::::::::::	100
MTL2	::::::::::::::::::::::::::::::::::::::	100
MTL3	::::::::::::::::::::::::::::::::::::::	100
MXMT1	DLFONDFNSVFKLLPSFYRKLEKENCRKIGSCLLSAMFCSFYCRLFPEES	149
MTL1	;;;;;;;;::::::::::::::::::::::::::::::	150
MTL2	::::::::::::::::::::::::::::::::::::::	150
MTL3	:::P::::::::::::::::::::::::::::::::::	150
MXMT1	MHFT.HSCYSVHWLSQVPSCELVTELGTGAVKCSTYSSKGCRPFVQKAYIDQ	199
MTL1	::::::S:::LQF:::::::T::::R::::::ASP:::::::	200
MTL2	::::::S:::LQF:::::::T::::T::::R::::::ASP:::::::	200
MTL3	::::::::CLQ::::::::T:::::ST:::::::::::::::::::AS:L::::::::::	200
MXMT1	FTKDFTFERIHSKELFSRÆMLÆGICKVÖEFDERVELDLLDMAINDLI	
MTL1	::::::::::::::::::::::::::::::::::::::	
MTL2	::::::::::::::::::::::::::::::::::::::	
MTL3	::::::::::::::::::::::::::::::::::::::	250
MXMT1	VBGLLEBEKLDSFNIPFFTPSADEVKCIVEEEGSCEILYLEIFKAHYDAA	
MTL1	A::R:G:::::::V:IY:A:V:::::M::::::F:::::Q:::IR:::G	
MTL2	:::H::::::::::::::::::::::::::::::::::	
MTL3	:::H:::::::L:VYI:::::::F::::::VL:::G	300
MXMT1	FSIDIDYPVRSH	
MTL1	:::::O::::SFVYSD:HAR:AH::::::::::::::::::::::::::::::::	
MTL2	:::::Q::::SPEYSD:HAR;AH::::L::::::N:::::I::I	
MTL3	::::: EH ::::::SV:A:::::::::::::::::::::::::::::	337
MXMT1	FHRLAKHAAKVIHMEKOCYNNLIISLAKKPEKSDV 378	٠.
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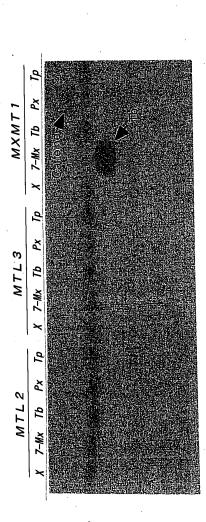
E: THEOBROMINE SYNTHASE POLYPEPTIDE
PLANT AND THE GENE ENCODING SAID POLYPEPTIDE
INVENTOR(S): HIROSHI SANO ET AL
APPLICATION SERIAL NO: UNASSIGNED
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FIG. 4



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INVENTOR(S): HIROSHI SANO, ET-AL

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FIG. 6

